



Correspondence

Universal genetic assessment for women with ovarian cancer not yet achieved: The promises of universal tumor DNA testing

To the editor

Recently, a systematic review and meta-analysis by Lin et al. (Lin, 2021) highlighted that genetic testing rates for women with ovarian cancer remain poor, and the effects of several interventions were reported. We truly appreciate the authors efforts on combining existing literature in an important overview to emphasize that women with ovarian cancer are not yet universally genetically tested in spite of recommendations. We wish to elaborate on the intervention of reflex *BRCA1/2* tumor testing as the effectivity of this intervention as presented in the article might lead to misinterpretation.

Lin et al. (Lin, 2021) identified two articles that report on the intervention of reflex *BRCA1/2* tumor testing in women with ovarian cancer. Their meta-analysis presents the collective effectivity of the intervention in terms of genetic testing completion rates. However, this is misleading as the articles implemented reflex *BRCA1/2* tumor testing for different primary objectives and hence present results for different outcomes. To clarify, McCuaig et al. (McCuaig, 2020) investigated the implementation of *BRCA1/2* tumor testing complementary to universal germline testing for all women with high-grade serous ovarian cancer. In contrast, Vos et al. (Vos, 2019) investigated reflex tumor *BRCA1/2* testing of all newly diagnosed epithelial ovarian cancer patients as a prescreen for both germline testing and treatment eligibility, with completion rate of testing of over 80%. Only those patients with an aberrant tumor *BRCA1/2* test (17%) require genetic counseling and germline testing. Indeed, around 90% of these patients chose for a germline genetic test and 57% were found to have hereditary ovarian cancer.

We have shown in daily practice that there are several advantages to using reflex *BRCA1/2* tumor testing of ovarian cancer as a prescreen (a Tumor-First approach) to germline testing. It is an effective method to tailor genetic counseling and germline testing to those women with a higher risk of a hereditary pathogenic variant. Additionally, the workflow reduces the number of patients that are tested both on tumor and germline DNA. Furthermore, it might reduce the uneven distribution of genetic testing rates among people with varying ethnicities or educational levels currently present (Lin, 2021). In our experience, the tumor *BRCA1/2* test can successfully be expanded to include other ovarian cancer risk genes.

Overall, we appreciate that Lin et al. (Lin, 2021) confirmed that we have not yet achieved universal genetic assessment for women with ovarian cancer, however we would like to stress that reflex *BRCA1/2*

tumor testing as a prescreen for a germline genetic test is much more effective in reaching this goal than they present and can be considered as a very useful approach.

Author contributions

All authors contributed to the writing of this letter, and have approved the final version.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

- Lin, J., et al., 2021. Achieving universal genetic assessment for women with ovarian cancer: Are we there yet? A systematic review and meta-analysis. *Gynecol. Oncol.* <https://doi.org/10.1016/j.ygyno.2021.05.011>.
- McCuaig, J.M., et al., 2020. Year 1: Experiences of a tertiary cancer centre following implementation of reflex *BRCA1* and *BRCA2* tumor testing for all high-grade serous ovarian cancers in a universal healthcare system. *Gynecol. Oncol.* 158 (3), 747–753. <https://doi.org/10.1016/j.ygyno.2020.06.507>.
- Vos, J.R., et al., 2019. Universal Tumor DNA *BRCA1/2* Testing of Ovarian Cancer: Prescreening PARPi Treatment and Genetic Predisposition. *JNCI: J. Natl. Cancer Inst.* 112 (2), 161–169. <https://doi.org/10.1093/jnci/djz080>.

Vera M. Witjes^a, Janet R. Vos^b, Marjolijn J.L. Ligtenberg^{a,c},
Nicoline Hoogerbrugge^{a,*}

^a Department of Human Genetics, Radboud Institute for Molecular Life Sciences, Radboud University Medical Center, Nijmegen, the Netherlands

^b Department of Human Genetics, Radboud Institute for Health Sciences, Radboud University Medical Center, Nijmegen, the Netherlands

^c Department of Pathology, Radboud Institute for Molecular Life Sciences, Radboud University Medical Center, Nijmegen, the Netherlands

* Corresponding author at: Department of Human Genetics, Radboud University Medical Center, PO Box 9101, 6500 HB Nijmegen, the Netherlands.

E-mail address: nicoline.hoogerbrugge@radboudumc.nl (N. Hoogerbrugge).

<https://doi.org/10.1016/j.gore.2021.100825>

Received 17 June 2021; Accepted 27 June 2021

Available online 30 June 2021

2352-5789/© 2021 The Authors.

Published by Elsevier Inc.

This is an open access article under the CC BY-NC-ND license

(<http://creativecommons.org/licenses/by-nc-nd/4.0/>).